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Minimum
Maximum
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                                                                                                                                                                                                                                                                                                                                                              Sequence:
                                                                                                                                                                                                                                                                                                                                                                                      Title:
                                                                                                                                                                                                                                                                                                                                                                                                                                       Run
                                                                                                                                                                    Database
                                                                                                                                                                                                                  Post-processing: Minimum Match 0%
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                                                                                                                                                                                                                                                                                                                                        Scoring table:
                                                                                                                                                                                                                                                                                                                                                                           Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                              protein -
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DB
                                                                                                                                                                                                                                         seq length: 0 seq length: 2000000000
                                                                                                                                                                                                                                                                                                                                                                                                                                                           protein search, using sw model
4:
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113:
14:
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53
1 CXXXCXXXXXXXXXXXXXXXXXX
                                                                                                                                                                  SPTREMBL_15:*
                                                                                                                                                                                          Maximum Match 100%
Listing first 45 su
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Gapop 10.0 ,
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          sp_fodent:*
sp_virus:*
sp_vertebrate:*
                                                                                                                                           sp_archea:*
sp_bacteria:*
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                                                                   sp_organelle:*
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Compugen Ltd
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27.919 Million cell updates/sec
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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19	18	17	16	15	14	13	12	11	10	9	8	7	Ø	J	4	w	2	1	Result No.
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Q9U341	Q94162	077729	077091	Q67593	072913	Q9JM45	Q16274	Q9N0X1	Q9VIA1	062555	062554	Q9VI99	041097	Q9M402	Q9U623	016861	077493	077490	ID
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		077729 ovis aries	077091 mesobuthus	Q67593 miscanthus		Q9jm45 mus musculu	Q16274 homo sapien	Q9n0x1 oryctolagus	Q9vial drosophila	062555 mytilus edu	062554 mytilus edu	Q9vi99 drosophila	041097 paramecium	Q9m402 glycine max	Q9u623 pacifastacu	Q16861 homo sapien	077493 lemur catta	077490 galago cras	Description

ALIGNMENTS

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RESULT 1
077490
ID 077490;
ID 077490;
AC 077490;
DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
DT 01-NOV-1998 (TREMBLrel. 08, Last annotation update)
DT 01-NOV-1998 (TREMBLREL 08, Last annotation update)
DT 01-NOV-1998 (TREMBLREL 08, Last annotation update)
DT 01-NOV-1998 (TREMBLREL 08, Last annotation update)
OS Galago crassicaudatus (Thick-tailed galago) (Otolemur crassicaudatus).
Rukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Rukaryota; Metazoa; Chordata; Strepsirhini; Galagonidae; Otolemur.
     AC DT DT DT DT DT DT DT
                                                                                        RESULT
077493
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Best Local Similarity 19.0
Conservative
              077493;
077493;
01-NOV-1998
01-NOV-1998
01-NOV-1998
D4 DOPAMINE
                                                                                                                                                                                                                                                                  NON_TER
                                                                                                                                                                                                                                                                                           receptor genes.";
Primates 39:217-224(1998).
EMBL; AB016199; BAA32037.1;
   Lemur catta
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8 (TrEMBLrel. 08, Created)
8 (TrEMBLrel. 08, Last seque
18 (TrEMBLrel. 08, Last annot
1E RECEPTOR (D4DR) (FRAGMENT)
2 (Ring-tailed lemur).
                                                                                                                                                                                                                                                       32 AA;
                                                                            PRELIMINARY;
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3157 MW; F492F6F29C2C5CEC CRC64;
                                                                                                                                                                                                    100.0%; Score 53; D
19.0%; Pred. No. 61;
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                                                                                                                                                                21
           (FRAGMENT).
                        Last sequence update)
Last annotation update)
                                                                            PRT;
                                                                                                                                                                                          Mismatches
                                                                            32
                                                                           AA
                                                                                                                                                                                                                DB 6; Length 32;
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RESULT ID (1686)
ID (2000)
DT (1000)
   RESULT RE
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Best Local S
Matches 4
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Best Local
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Q9U623;
Q1-MAY-2000 (TrEMBLrel. 13,
01-MAY-2000 (TrEMBLrel. 13,
01-CT-2000 (TrEMBLrel. 15,
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SEQUENCE FROM N.A.
TISSUB-THORACIC GANGLIA;
SKORUPSKI P., Dawbarn D.;
Submitted (OCT-1999) to the
EMBL; AF199482; AAF07215.1;
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SEQUENCE
                                                                                                                                                                                                                               Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca; Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Astacidea; Astacidae; Pacifastacus.
                                                                                                                                                                                                                                                                                                                          METALLOTHIONEIN.
Pacifastacus leniusculus (Signal crayfish).
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                                                                                                                                                                                                   NCBI_TaxID=6720;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens (Human).
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Primates 39:217-224(1998).
EMBL: AB016202; BAA32040.1; -.
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Mammalia; Eutheria;
NCBI_TaxID=9447;
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"Origin and divergence of tandem repeats
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       11
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19.0%;
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01, Last sequence update)
07, Last annotation update)
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the EMBL/GenBank/DDBJ
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17; Mismatches
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RESULT
041097
  Query Match
Best Local Similarity
""" April 4; Conserv
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INTERPRO; IPR002045; -.
INTERPRO; IPR003019; -.
IPROM; PF00131; metalthio; 1.
PRINTS; PR00858; MTCRUSTACEAN.
SEQUENCE 58 AA; 6008 MW; 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Q9M402;
Q9M402;
01-OCT-2000
01-OCT-2000
01-OCT-2000
                                                                                                             O41097;
01-JAN-1998 (TrEMBLrel.
01-JAN-1998 (TrEMBLrel.
01-NOV-1998 (TrEMBLrel.
Li Y., Lu Z., Sun L., Ropp S., Kutish "Analysis of 74 kb of DNA located at t chlorella virus PBCV-1 genome.";
                                                   NCBI_Tax1D=10506;
[1]
                                                                                                                                                                                                                                                                                                Thesis (1998), University of Udine, EMBL; AJ276118; CABB3040.1; -.
NON TER 62 62
SEQUENCE 62 AA; 7158 MW; 10690b
                            SEQUENCE FROM N.A. MEDLINE=98022962;
                                                                      Paramecium
Viruses; ds
                                                                                           A615R.
                                                                                                     A615R PROTEIN.
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                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A. Morassutti C., Mar
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Glycine max (Soybean)
                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                     Submitted
                                                                                                                                                                                                                                                                                                                                                                     tobacco transgenic p. Submitted (MAR-2000)
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                                                                                                                                                                                                                                                                                                                                                                                                                                          Fabales;
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"Expression and purification of the antimicrobial 
tobacco transgenic plants by SceVMA-intein system. 
Submitted (MAR-2000) to the EMBL/GenBank/DDBJ data
                                                                                                                                                                                                        38 CLQSCNSERDSYRNQACHARC
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4; Conservative
                                                                      dsDNA
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                                                                    bursaria chlo
sDNA viruses,
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                              PubMed=9356347;
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Lrel. 15, Last annotation update)
BETA-CONGLYCININ (FRAGMENT).
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dons; core eudicots; Rosidae;
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Last annotation update)
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Phycodnaviridae;
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e; eurosids I;
          , Van Etten J.L.;
the 330-kb
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                                                                     Phycodnavirus
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01-MAY-2000
01-JUN-2000
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EMBL; U42580; AAC97026.1; -.
SEQUENCE 66 AA; 7112 MW;
                                   "The genome sequence of Drosophila Science 287:2185-2195(2000). EMBL; AE003672; AAF54026.1; -.
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                                                                              melanogaster.";
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062555;
01-AUG-1998
01-AUG-1998
01-OCT-2000
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01-AUG-1998
01-OCT-2000
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                                                       Barsyte D., White K.N., Low Submitted (APR-1998) to the EMBL; AJ005453; CAA06550.1;
                                                                                                                                    Mytilus edulis (Blue mussel).
Eukaryota; Metazoa; Mollusca;
                                                                                                                                                                                                                                                                                                                                               PRINTS; PR00875; MTMOLLUSC.
PROSITE; PS00022; EGF_1; UNKNOWN_1
SEQUENCE 73 AA; 7220 MW; 767971
                                                                                                                                                                                                                                                                                                                                                                                                                            Barsyte D., White K.N., Lovejoy D.A.;
Submitted (APR-1998) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
TISSUE=DIGESTIVE GLAND;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mytiloidea; Mytilidae;
NCBI_TaxID=6550;
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SEQUENCE 72 AA; 6840 MW; 8CE37449E5F88ABA
         PRINTS; PR00875; MTMOLLUSC
                   PFAM; PF00131; metalthio;
                                                                                       TISSUE=DIGESTIVE GLAND;
                                                                                                SEQUENCE FROM N.A.
                                                                                                                   NCBI_TaxID=6550;
                                                                                                                              Mytiloidea;
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                                                                                                                                                                                                                                                                                                                                                                                                                    AJ005452; CAA06549.1;
                                                                                                                                                                                                                                                                                              4; Conserv
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4; Conservative
 PS00022;
                            IPR003019; -
                                      IPR000561; -.
                                                                                                                                                                                                                                                                                                                                                                                                         IPR000561;
                                                                                                                                                                                                                                                                                                                                                                                                IPR001008; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Metazoa; Mollusca;
                                                                                                                             Mytilidae;
                                                                                                                                                                  (TrEMBLrel. 07,
(TrEMBLrel. 07,
(TrEMBLrel. 15,
                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                         PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRELIMINARY;
EGF_1; UNKNOWN_1.
                                                                                                                                                                                                                                                                                                         19.0%;
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                                                                                                                             Mytilus
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                                                                             Lovejoy
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Pred. No.
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                                                                   EMBL/GenBank/DDBJ databases
                                                                                                                                                                          Last sequence update)
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Pred. No.
                                                                                                                                                                  Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                76797FB0FCD7B3B2 CRC64;
                                                                                                                                      Bivalvia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bivalvia;
                                                                                                                                                                                                         PRT;
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                                                                             D.A.;
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                                                                                                                                                                                                                                                                                                                  53;
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                                                                                                                                                                                                                                                                                                         98;
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                                                                                                                                     Pteriomorphia; Mytiloida;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pteriomorphia; Mytiloida;
                                                                                                                                                                                                         AΑ
                                                                                                                                                                                                                                                                                                                   DB 5;
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SO

SEQUENCE

73

AA;

7153 MW;

20CFA4CB3A0CDE19 CRC64;

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RESULT
Q9VIA1
                                                                  RA Ballew R.M. Basu A. Basunah B.P. Andrews-trannoch C. Baldwin D., RA Ballew R.M. Basu A. Basunah B.P. Bhandari D. Bolshakov S. RA Besson K.Y. Benos P.V., Berman B.P. Bhandari D., Bolshakov S. RA Cherry J.M. Cawley S., Dutler H., Caddeu E., Center A., Chandra I., RA de Pablos B., Delcher A., Dang Z., Mays A.D., Dew I., Dietz S.M., RA de Pablos B., Delcher A., Dong Z., Mays A.D., Dew I., Dietz S.M., RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P., RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P., RA Posler C., Gabrielian A.E., Garg N.S., Gelbart M.M., Glasser K., RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M., RA Horris N.L., Harvey D., Heiman T.J., Wei M.-H., Ibeyamm C.J., Harvey D., Heiman T.J., Wei M.-H., Ibeyamm C.J., RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibeyamm C.J., Kallahi M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A., RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPharson D. A., Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A., RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPharson D. L., RA Mensulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A., RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M., Ra Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G., RA Ra Mensulov G., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T., RA Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J., Ra Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J., Ra Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J., Ra Wang X.H., Zhong W., Zhon M., Zhang G., Zhao Q., Zheng L., Rhong X., Ersendons Sequence of Drosophila melanogaster.";

BOR Pathological P. McGlasser J. Schu X., Smith H.O., RABLI AROJSOL A.F., Sunfishob.
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ephydroidea; Drc
NCBI_TaxID=7227;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pterygota; Neoptera; Endopterygota; Diptera; Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MST84DB
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01-JUN-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=20196006; PubMed=10731132;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM
                                         INTERPRO;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       26 CGDACKCSGADCKCSGCKVVC 46
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PS00198;
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                                                       FBgn0004173; Mst84Db
                                       IPR001450;
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4FE4S_FERREDOXIN; UNKNOWN_4.
6725 MW; CC64F0F7A7E7CABC CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      100.0%;
19.0%;
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Last annotation updat
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Pred. No. 98;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0;
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RESULT
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Q16274;
Q1-0074;
Q1-NOV-1996 (TrEMBLrel. 01,
Q1-NOV-1996 (TrEMBLrel. 01,
Q1-MAY-2000 (TrEMBLrel. 13,
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NON_TER
SEQUENCE
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O9NOX1, 01-OCT-2000 (TrEMBLrel. 15,
01-OCT-2000 (TrEMBLrel. 15,
01-OCT-2000 (TrEMBLrel. 15,
                                                                                  Bowden P.E.,
J. Dermatol.
                                                                                                                          Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
MCBI_TaxID=9606;
                                                                                                                                                           Homo sapiens (Human)
                                                                                                                                                                    TYPE II HAIR KERATIN (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PUTATIVE EPIDERMAL GROWTH FACTOR RECEPTOR (FRAGMENT).
Oryctolagus cuniculus (Rabbit) Craniata; Vertebrata; Euteleostomi;
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
SEQUENCE
           NON_TER
                              PROSITE;
                                        PFAM; PF00038; filament; 1.
                                                              EMBL;
                                                                                            Bowden P.
                                                                                                       SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                 Submitted (MAR-2000) to the EMBL; AF243516; AAF65771.1;
                    Intermediate
                                                           -!- SIMILARITY: TO ALL OTHER INTERMEDIATE FILAMENT PROTEINS EMBL; S75796; AAB32813.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                             TISSUE=SCLERA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=9986;
                                                                                                                                                                                                                                                                                                                                                                                                       Receptor.
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                                                    NTERPRO;
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                               PS00226;
                                                                                                       FROM N.A.
                                                   IPR001664; -
81
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                                                                                                                                                                                                                                                                                                                     Conservative
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                                                                                  Sci.
                   filament;
                                                                                  Hainey S., Parker G., Sci. 0:0-0(1994).
AA;
           ; IF; 1.
8244 MW;
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8155
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                                                                                                                                                                              Last sequence update)
Last annotation update)
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5F0A3D7735A5B03C CRC64;
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Pred. No.
                                                                                                                                      Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
                   coil; Heptad
                                                                                                                                                                                                                          PRT;
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                                                                                           Hodgins M.B.;
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                   repeat pattern
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Query Match Best Local Similarity

100.0%; 19.0%;

Score 53; DB 4 Pred. No. 1e+02;

4

Length 81;

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RESULT 15
Q67593
ID Q67593
AC Q67593
DT 01-NOV
DT 01-NOV
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Q9JM45
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Best Local S
Matches 4
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Best Local Similarity
Matches 4; Conserv
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 Q67593;
Q67593;
Q1-NOV-1996
Q1-NOV-1996
Q1-NOV-1998
                                                                                                                                                                                                                                                                                                         072913;
072913;
01-AUG-1998
01-AUG-1998
01-AUG-1998
                                                                                                                                                                                        Sugimoto K., Hirochika H., Minobe Y., Kawamata H., Hibi Yamashita S., Tsuchizaki T.; Submitted (AUG-1992) to the EMBL/GenBank/DDBJ databases. EMBL; D00800; BAA25577.1; - SEQUENCE 84 AA; 8721 MW; B57A04C249776B1C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.

Jin C., Lau A.F.;
Submitted (DEC-1997) to the EMBL/GenBank/DDBJ databases EMBL; AF038507; AAF28736.1; -.
SEQUENCE 83 AA; 8909 MW; 275B78E46428A3DE CRC64;
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01-OCT-2000 (TrEMBLrel.
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Viruses; ssDNA viruses; Geminiviridae;
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Eukaryota; Metazoa; Chordata;
Mammalla; Eutheria; Rodentia;
NCBI_TaxID=10090;
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                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
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19.0%; Pr
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Best Local Similarity
Matches 4; Conser
                                                                                              "The nucleotide sequence and genome structure of Geminivirus Miscanthus streak virus.";
Submitted (DEC-1991) to the EMBL/GenBank/DDBJ databases.
EMBL; D01030; BAA00837.1; -.
SEQUENCE 84 AA; 8751 MW; A8CCDFB249776BIC CRC64;
                                                                                                                                                                                                Viruses; ssDNA viruses; NCBI_TaxID=10825;
                                                                                                                                                      Davies J.W.;
                                                                                                                                                                Chatani M., Matsumoto Y., Mizuta H.,
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Miscanthus streak virus
                                                                                                                                                                            SEQUENCE FROM N.A.
 28
                 1 CXXXCXXXXXXXXXXXXX 21
CLIGCLWAAYRLFLKECLTDC
                                          Conservative
                                                  100.0%;
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                                                    .0%; Score 53
                                          Mismatches
                                                    53;
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                                                    DB 12;
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                                                              Length
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Search completed: March 1, 2001, 16:22:08 Job time: 285 sec

